

09/980862

JC10 Rec'd PCT/PTC 07 DEC 2001

1

## SEQUENCE LISTINGS

<110> Skerra, Arne, Prof. Dr.

5 <120> Muteins of bilin-binding protein

<150> DE 199 26 068.0

<151> 1999-06-08

10 <160> 18

<210> 1

<211> 1219 base pairs

<212> DNA

15 <213> artificial sequence

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<221> sig\_peptide

<222> (22)...(84)

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<221> mat\_peptide

<222> (85)...(1209)

<223> fusion protein of bilin-binding protein, Strep-tag II und fragment

25 of phage coat protein pIII

<220>

<221> CDS

<222> (85)...(606)

30 <223> mature bilin-binding protein

<220>

<221> CDS

<222> (607)...(636)

35 <223> Strep-tag II-affinity tag

<220>

<221> CDS

<222> (637)...(639)

<223> amber stop codon

<220>

5 <221> CDS

<222> (640)...(1209)

<223> amino acids 217-406 of coat protein pIII

<400> 1

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      -21 -20                      -15

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      Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val
      -10                      -5          -1  1

20  TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC 135
      Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe
      5                      10          15

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      Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
      20                      25          30

30  CCC AAC TCA GTT GAG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC 225
      Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr
      35                      40          45

35  ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC 270
      Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile
      50                      55          60

40  CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT 315
      His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly
      65                      70          75

45  GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT 360
      Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly
      80                      85          90

50  GTC ACC AAG GAG AAC GTA TTC AAC GTA CTC TCC ACT GAC AAC AAG 405
      Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
      95                      100         105

      AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG 450
      Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys
      110                      115         120

      GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT 495
      Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu
      125                      130         135

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	ACT	GGT	GAA	GCC	AAG	ACC	GCT	GTC	GAG	AAC	TAC	CTT	ATC	GGC	TCC	540
	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	
			140					145					150			
5	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
10	GCC	GCC	TGC	AAG	GTC	AAC	AAT	AGC	AAC	TGG	TCT	CAC	CCG	CAG	TTC	630
	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
15	GAA	AAA	TAG	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGC	GGC	GGC	675
	Glu	Lys	Gln	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
			185					190					195			
20	TCT	GAG	GGT	GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	720
	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	
			200					205					210			
	TCT	GAG	GGA	GGC	GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	765
	Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	
			215					220					225			
25	GAT	TAT	GAA	AAG	ATG	GCA	AAC	GCT	AAT	AAG	GGG	GCT	ATG	ACC	GAA	810
	Asp	Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	
			230					235					240			
30	AAT	GCC	GAT	GAA	AAC	GCG	CTA	CAG	TCT	GAC	GCT	AAA	GGC	AAA	CTT	855
	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	
			245					250					255			
35	GAT	TCT	GTC	GCT	ACT	GAT	TAC	GGT	GCT	GCT	ATC	GAT	GGT	TTC	ATT	900
	Asp	Ser	Val	Ala	Thr	Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	
			260					265					270			
40	GGT	GAC	GTT	TCC	GGC	CTT	GCT	AAT	GGT	AAT	GGT	GCT	ACT	GGT	GAT	945
	Gly	Asp	Val	Ser	Gly	Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	
			275					280					285			
	TTT	GCT	GGC	TCT	AAT	TCC	CAA	ATG	GCT	CAA	GTC	GGT	GAC	GGT	GAT	990
	Phe	Ala	Gly	Ser	Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	
			290					295					300			
45	AAT	TCA	CCT	TTA	ATG	AAT	AAT	TTC	CGT	CAA	TAT	TTA	CCT	TCC	CTC	1035
	Asn	Ser	Pro	Leu	Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	
			305					310					315			
50	CCT	CAA	TCG	GTT	GAA	TGT	CGC	CCT	TTT	GTC	TTT	GGC	GCT	GGT	AAA	1080
	Pro	Gln	Ser	Val	Glu	Cys	Arg	Pro	Phe	Val	Phe	Gly	Ala	Gly	Lys	
			320					325					330			
55	CCA	TAT	GAA	TTT	TCT	ATT	GAT	TGT	GAC	AAA	ATA	AAC	TTA	TTC	CGT	1125
	Pro	Tyr	Glu	Phe	Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	
			335					340					345			
60	GGT	GTC	TTT	GCG	TTT	CTT	TTA	TAT	GTT	GCC	ACC	TTT	ATG	TAT	GTA	1170
	Gly	Val	Phe	Ala	Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	
			350					355					360			

TTT TCT ACG TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT 1209  
 Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
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5 TAATAAGCTT 1219

<210> 2

<211> 64 bases

10 <212> DNA

<213> artificial sequence

<220>

<223> primer

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<400> 2

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 ACGGAAAGTG CGGA 64

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<210> 3

<211> 71 bases

<212> DNA

25 <213> artificial sequence

<220>

<223> primer

30 <400> 3

GGGTAGGCGG TACCTTCSNN AAAGTATTCC TTGCCGTGGA TTACMNGTA 50  
 SNNCGAAACT TTGACACTCT T 71

35

<210> 4

<211> 74 bases

<212> DNA

<213> artificial sequence

40

<220>

<223> primer

$\langle 400 \rangle$  4

5 CCAAGATTGG AAAGATCTAC CACAGCNNSA CTNNKGAGG TNSACC VVS 50  
GAGNNKG TAT TCAACGTACT CTCC 74

<210> 5

<211> 78 bases

10 <212> DNA

<213> artificial sequence

$\langle 220 \rangle$

<223> primer

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<400> 5

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<210> 6

<211> 36 bases

<212> DNA

<213> artificial sequence

25

 $\langle 220 \rangle$ 

<223> primer

<400> 6

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<210> 7

35 <211> 37 bases

<212> DNA

<213> artificial sequence

 $\langle 220 \rangle$

<223> primer

<400> 7

CACCAGTAAG GACCATGCTT CTGGAGAGCA CCCAGAC 37

5

<210> 8

<211> 46 bases

<212> DNA

<213> artificial sequence

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 $\langle 220 \rangle$ 

<223> synthetic oligodeonucleotide

<400> 8

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<210> 9

<211> 793 base pairs

20 <212> DNA

<213> fragment of plasmid pBBP22

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<221> sig_peptide
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25  $\langle 222 \rangle$  (22) ... (84)

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<221> mat_peptide
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<222> (85) ... (783)

30 <223> fusion protein of bilin-binding protein, Strep-Tag II und albumin-binding domain

 $\langle 220 \rangle$ 

<221> CDS

35  $\langle 222 \rangle$  (85) ... (606)

<223> mature bilin-binding protein

AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG 450  
Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys  
110 115 120

GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT 495  
 Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu  
 125 130 135

5 ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC GGC TCC 540  
 Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser  
 140 145 150

10 CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC TCT GAA 585  
 Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu  
 155 160 165

15 GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT CAC CCG CAG TTC 630  
 Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe  
 170 175 180

GAA AAA CCA GCT AGC CTG GCT GAA GCT AAA GTT CTG GCT AAC CGT 675  
 Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg  
 185 190 195

20 GAA CTG GAC AAA TAC GGT GTT TCC GAC TAC TAC AAA AAC CTC ATC 720  
 Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile  
 200 205 210

25 AAC AAC GCT AAA ACC GTT GAA GGT GTT AAA GCT CTG ATC GAC GAA 765  
 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu  
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<210> 10

35 <211> 17 bases

<212> DNA

<213> artificial sequence

<220>

40 <223> sequencing primer

<400> 10

GACGGTGCCT GTCCCGA 17

45 <210> 11

<211> 17 bases

<212> DNA

<213> artificial sequence



<220>

<223> sequencing primer

<400> 11

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GACTACTGGG GAGCCGA 17

<210> 12

10 <211> 522 bases

<212> DNA

<213> coding sequence of mutein DigA

<220>

15 <221> CDS

<222> (1)...(522)

<223> mutein DigA without fusions parts

<400> 12

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1				5					10					15	

25

AAC	TTC	GAC	TGG	TCC	CAG	TAC	CAT	GGT	AAA	TGG	TGG	GAA	GTC	GCC	90
Asn	Phe	Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala	
				20					25					30	

30

AAA	TAC	CCC	CAT	CAC	GAG	CGG	AAG	TAC	GGA	AAG	TGC	GGA	TGG	GCT	135
Lys	Tyr	Pro	His	His	Glu	Arg	Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	
				35					40					45	

35

GAG	TAC	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	CGC	TAC	TCT	180
Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Arg	Tyr	Ser	
				50					55					60	

40

GTA	ATC	CAC	GGC	AAG	GAA	TAC	TTT	TCC	GAA	GGT	ACC	GCC	TAC	CCA	225
Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ser	Glu	Gly	Thr	Ala	Tyr	Pro	
				65					70					75	

45

GTT	GGT	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	TAC	ACT	ATT	270
Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Tyr	Thr	Ile	
				80					85					90	

45

GGA	GGT	GTG	ACC	CAG	GAG	GGT	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	315
Gly	Gly	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	
				95					100					105	

10

AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC GAG GAC 360  
 Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp  
 110 115 120

5 AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA AGC ATG 405  
 Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met  
 125 130 135

10 GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC 450  
 Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile  
 140 145 150

15 GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC 495  
 Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
 155 160 165

TCT GAA GCC GCC TGC AAG GTC AAC AAT 522  
 Ser Glu Ala Ala Cys Lys Val Asn Asn  
 170

20

&lt;210&gt; 13

&lt;211&gt; 76 bases

&lt;212&gt; DNA

25 &lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; primer

30 &lt;400&gt; 13

CTGGTCCCAG TACCATGGTA AATGGTGGNN KGTCGCCNNK TACCCCNKN 50  
 NKNNKNNKAA GTACGGAAAG TGCGGA 76

35

&lt;210&gt; 14

&lt;211&gt; 1219 bases pairs

&lt;212&gt; DNA

&lt;213&gt; fragment of phasmids pBBP24

40

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (22)...(84)

<220>

<221> mat\_peptide

<222> (85)...(1209)

<223> fusion protein of bilin-binding protein, Strep-Tag II and fragment  
5 of phage coat protein pIII, with interrupted reading frame

<220>

<221> CDS

<222> (85)...(606)

10 <223> mature bilin-binding protein with interrupted reading frame

<220>

<221> CDS

<222> (607)...(636)

15 <223> Strep-Tag II affinity tag

<220>

<221> CDS

<222> (637)...(639)

20 <223> amber stop codon

<220>

<221> CDS

<222> (640)...(1209)

25 <223> amino acids 217-406 of coat protein pIII

<400> 14

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	Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val	
	-10 -5 -1 1	
40	TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC	135
	Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe	
	5 10 15	
	GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC	180
	Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr	
	20 25 30	

	CCC	AAC	TCA	GTT	GAG	AAG	TAC	GGA	AAT	TAA	TGA	TGG	GCT	GAG	TAC	225
	Pro	Asn	Ser	Val	Glu	Lys	Tyr	Gly	Asn			Trp	Ala	Glu	Tyr	
			35					40					45			
5	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	AAC	TAC	CAC	GTA	ATC	270
	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Asn	Tyr	His	Val	Ile	
			50					55					60			
10	CAC	GGC	AAG	GAA	TAC	TTT	ATT	GAA	GGA	ACT	GCC	TAC	CCA	GTT	GGT	315
	His	Gly	Lys	Glu	Tyr	Phe	Ile	Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	
			65					70					75			
15	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	CTG	ACT	TAC	GGA	GGT	360
	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Leu	Thr	Tyr	Gly	Gly	
			80					85					90			
20	GTC	ACC	AAG	GAG	AAC	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	AAC	AAG	405
	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys	
			95					100					105			
25	AAC	TAC	ATC	ATC	GGA	TAC	TAC	TGC	AAA	TAC	GAC	GAG	GAC	AAG	AAG	450
	Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	Asp	Glu	Asp	Lys	Lys	
			110					115					120			
30	GGA	CAC	CAA	GAC	TTC	GTC	TGG	GTG	CTC	TCC	AGA	AGC	ATG	GTC	CTT	495
	Gly	His	Gln	Asp	Phe	Val	Trp	Val	Leu	Ser	Arg	Ser	Met	Val	Leu	
			125					130					135			
35	ACT	GGT	GAA	GCC	AAG	ACC	GCT	GTC	GAG	AAC	TAC	CTT	ATC	GGC	TCC	540
	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	
			140					145					150			
40	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
45	GCC	GCC	TGC	AAG	GTC	AAC	AAT	AGC	AAC	TGG	TCT	CAC	CCG	CAG	TTC	630
	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
50	GAA	AAA	TAG	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGC	GGC	GGC	675
	Glu	Lys	Gln	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
			185					190					195			
55	TCT	GAG	GGT	GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	720
	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	
			200					205					210			
60	TCT	GAG	GGA	GGC	GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	765
	Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	
			215					220					225			
65	GAT	TAT	GAA	AAG	ATG	GCA	AAC	GCT	AAT	AAG	GGG	GCT	ATG	ACC	GAA	810
	Asp	Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	
			230					235					240			
70	AAT	GCC	GAT	GAA	AAC	GCG	CTA	CAG	TCT	GAC	GCT	AAA	GGC	AAA	CTT	855
	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	
			245					250					255			

50    GAC GTG TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC    45  
      Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp

14

	1	5	10	15	
	AAC TTC GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG GTC GCC	90			
5	Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala	30			
		20	25	30	
	GCG TAC CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA TGG GCT	135			
10	Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala	45			
		35	40	45	
	GAG TAC ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG CGC TAC TCT	180			
	Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser	60			
		50	55	60	
15	GTA ATC CAC GGC AAG GAA TAC TTT TCC GAA GGT ACC GCC TAC CCA	225			
	Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro	75			
		65	70	75	
	GTT GGT GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC TAC ACT ATT	270			
20	Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile	90			
		80	85	90	
	GGA GGT GTG ACC CAG GAG GGT GTA TTC AAC GTA CTC TCC ACT GAC	315			
25	Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp	105			
		95	100	105	
	AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC GAG GAC	360			
30	Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp	120			
		110	115	120	
	AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA AGC ATG	405			
	Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met	135			
		125	130	135	
35	GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC	450			
	Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile	150			
		140	145	150	
	GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC	495			
40	Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	165			
		155	160	165	
	TCT GAA GCC GCC TGC AAG GTC AAC AAT	522			
45	Ser Glu Ala Ala Cys Lys Val Asn Asn	170			

&lt;210&gt; 16

&lt;211&gt; 1380 base pairs

50 &lt;212&gt; DNA

&lt;213&gt; fragment of plasmids PBBP21

&lt;220&gt;

&lt;221&gt; sig\_peptide

<222> (22)...(84)

<220>

<221> mat\_peptide

5 <222> (85)...(636)

<223> fusion protein of bilin-binding protein and Strep-Tag II

<220>

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10 <222> (658)...(717)

<220>

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<222> (718)...(1365)

15 <223> DsbC protein

<400> 16

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	Met Lys Lys Thr Ala Ile Ala Ile	
	-21 -20 -15	
25	GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GAC GTG	90
	Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val	
	-10 -5 -1 1	
30	TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC	135
	Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe	
	5 10 15	
35	GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC	180
	Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr	
	20 25 30	
40	CCC AAC TCA GTT GAG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC	225
	Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr	
	35 40 45	
45	ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC	270
	Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile	
	50 55 60	
50	CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT	315
	His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly	
	65 70 75	
55	GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT	360
	Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly	
	80 85 90	

	GTC ACC AAG GAG AAC GTA TTC AAC GTA CTC TCC ACT GAC AAC AAG	405
	Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys	
	95 100 105	
5	AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG	450
	Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys	
	110 115 120	
10	GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT	495
	Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu	
	125 130 135	
15	ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC GGC TCC	540
	Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser	
	140 145 150	
20	CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC TCT GAA	585
	Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu	
	155 160 165	
	GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT CAC CCG CAG TTC	630
	Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe	
	170 175 180	
25	GAA AAA TAATAAGCTT CGGGAAGATT T ATG AAG AAA GGT TTT ATG	675
	Glu Lys Met Lys Lys Gly Phe Met	
	-20 -15	
30	TTG TTT ACT TTG TTA GCG GCG TTT TCA GGC TTT GCT CAG GCT GAT	720
	Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly Phe Ala Gln Ala Asp	
	-10 -5 -1 1	
35	GAC GCG GCA ATT CAA CAA ACG TTA GCC AAA ATG GGC ATC AAA AGC	765
	Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser	
	5 10 15	
40	AGC GAT ATT CAG CCC GCG CCT GTA GCT GGC ATG AAG ACA GTT CTG	810
	Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu	
	20 25 30	
45	ACT AAC AGC GGC GTG TTG TAC ATC ACC GAT GAT GGT AAA CAT ATC	855
	Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile	
	35 40 45	
	ATT CAG GGG CCA ATG TAT GAC GTT AGT GGC ACG GCT CCG GTC AAT	900
	Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val Asn	
	50 55 60	
50	GTC ACC AAT AAG ATG CTG TTA AAG CAG TTG AAT GCG CTT GAA AAA	945
	Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
	65 70 75	
55	GAG ATG ATC GTT TAT AAA GCG CCG CAG GAA AAA CAC GTC ATC ACC	990
	Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr	
	80 85 90	
60	GTG TTT ACT GAT ATT ACC TGT GGT TAC TGC CAC AAA CTG CAT GAG	1035
	Val Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu	
	95 100 105	



CAA ATG GCA GAC TAC AAC GCG CTG GGG ATC ACC GTG CGT TAT CTT 1080  
 Gln Met Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu  
 110 115 120  
 5  
 GCT TTC CCG CGC CAG GGG CTG GAC AGC GAT GCA GAG AAA GAA ATG 1125  
 Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met  
 125 130 135  
 10  
 AAA GCT ATC TGG TGT GCG AAA GAT AAA AAC AAA GCG TTT GAT GAT 1170  
 Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp  
 140 145 150  
 15  
 GTG ATG GCA GGT AAA AGC GTC GCA CCA GCC AGT TGC GAC GTG GAT 1215  
 Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys Asp Val Asp  
 155 160 165  
 20  
 ATT GCC GAC CAT TAC GCA CTT GGC GTC CAG CTT GGC GTT AGC GGT 1260  
 Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val Ser Gly  
 170 175 180  
 25  
 ACT CCG GCA GTT GTG CTG AGC AAT GGC ACA CTT GTT CCG GGT TAC 1305  
 Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu Val Pro Gly Tyr  
 185 190 195  
 30  
 CAG CCG CCG AAA GAG ATG AAA GAA TTC CTC GAC GAA CAC CAA AAA 1350  
 Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys  
 200 205 210  
 30  
 ATG ACC AGC GGT AAA TAATTCGCGT AGCTT 1380  
 Met Thr Ser Gly Lys  
 215

35

<210> 17  
 <211> 2009 bases pairs  
 <212> DNA  
 <213> fragment of plasmid PBBP27

40

<220>  
 <221> sig\_peptide  
 <222> (23)...(85)

45

<220>  
 <221> mat\_peptide  
 <222> (86)...(1999)  
 <223> fusion protein of alkaline phosphatase, linker peptide Pro-Pro-Ser-Ala, mutein DigA16 and Strep-Tag II

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (86)...(1435)

5 &lt;223&gt; mature part of alkaline phosphatase

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1436)...(1447)

10 &lt;223&gt; linker peptide Pro-Pro-Ser-Ala

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1448)...(1969)

15 &lt;223&gt; mutein DigA16

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1970)...(1999)

20 &lt;223&gt; Strep-Tag II affinity tag

&lt;400&gt; 17

25	TCTAGAACAT GGAGAAAATA AA GTG AAA CAA AGC ACT ATT GCA CTG	46
	Val Lys Gln Ser Thr Ile Ala Leu	
	-21 -20 -15	
30	GCA CTC TTA CCG TTA CTG TTT ACC CCT GTG ACA AAA GCC CGG ACA	91
	Ala Leu Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr	
	-10 -5 -1 1	
35	CCA GAA ATG CCT GTT CTG GAA AAC CGG GCT GCT CAG GGC GAT ATT	136
	Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile	
	5 10 15	
40	ACT GCA CCC GGC GGT GCT CGC CGT TTA ACG GGT GAT CAG ACT GCC	181
	Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala	
	20 25 30	
45	GCT CTG CGT GAT TCT CTT AGC GAT AAA CCT GCA AAA AAT ATT ATT	226
	Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile	
	35 40 45	
50	TTG CTG ATT GGC GAT GGG ATG GGG GAC TCG GAA ATT ACT GCC GCA	271
	Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala	
	50 55 60	

5	CGT AAT TAT GCC GAA GGT GCG GGC GGC TTT TTT AAA GGT ATA GAT 316	
	Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp 75	
10	GCC TTA CCG CTT ACC GGG CAA TAC ACT CAC TAT GCG CTG AAT AAA 361	
	Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys 90	
15	AAA ACC GGC AAA CCG GAC TAC GTC ACC GAC TCG GCT GCA TCA GCA 406	
	Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala 105	
20	ACC GCC TGG TCA ACC GGT GTC AAA ACC TAT AAC GGC GCG CTG GGC 451	
	Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly 120	
25	GTC GAT ATT CAC GAA AAA GAT CAC CCA ACG ATT CTG GAA ATG GCA 496	
	Val Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala 135	
30	AAA GCC GCA GGT CTG GCG ACC GGT AAC GTT TCT ACC GCA GAG TTG 541	
	Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu 150	
35	CAG GAT GCC ACG CCC GCT GCG CTG GTG GCA CAT GTG ACC TCG CGC 586	
	Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg 165	
40	AAA TGC TAC GGT CCG AGC GCG ACC AGT GAA AAA TGT CCG GGT AAC 631	
	Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn 180	
45	GCT CTG GAA AAA GGC GGA AAA GGA TCG ATT ACC GAA CAG CTG CTT 676	
	Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu 195	
50	AAC GCT CGT GCC GAC GTT ACG CTT GGC GGC GGC GCA AAA ACC TTT 721	
	Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe 210	
55	GCT GAA ACG GCA ACC GCT GGT GAA TGG CAG GGA AAA ACG CTG CGT 766	
	Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg 225	
60	GAA CAG GCA CAG GCG CGT GGT TAT CAG TTG GTG AGC GAT GCT GCC 811	
	Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala 240	
65	TCA CTG AAT TCG GTG ACG GAA GCG AAT CAG CAA AAA CCC CTG CTT 856	
	Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu 255	
70	GGC CTG TTT GCT GAC GGC AAT ATG CCA GTG CGC TGG CTA GGA CCG 901	
	Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro 270	
75	AAA GCA ACG TAC CAT GGC AAT ATC GAT AAG CCC GCA GTC ACC TGT 946	
	Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys 285	

	ACG CCA AAT CCG CAA CGT AAT GAC AGT GTA CCA ACC CTG GCG CAG	991
	Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln	
	290 295 300	
5	ATG ACC GAC AAA GCC ATT GAA TTG TTG AGT AAA AAT GAG AAA GGC	1036
	Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly	
	305 310 315	
10	TTT TTC CTG CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT CAT	1081
	Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His	
	320 325 330	
15	GCT GCG AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT CTC GAT	1126
	Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp	
	335 340 345	
20	GAA GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG GAG GGT AAC	1171
	Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn	
	350 355 360	
	ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC CAC GCC AGC CAG ATT	1216
	Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile	
	365 370 375	
25	GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ACC CAG GCG CTA AAT	1261
	Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn	
	380 385 390	
30	ACC AAA GAT GGC GCA GTG ATG GTG ATG AGT TAC GGG AAC TCC GAA	1306
	Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu	
	395 400 405	
35	GAG GAT TCA CAA GAA CAT ACC GGC AGT CAG TTG CGT ATT GCG GCG	1351
	Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala	
	410 415 420	
40	TAT GGC CCG CAT GCC GCC AAT GTT GTT GGA CTG ACC GAC CAG ACC	1396
	Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr	
	425 430 435	
45	GAT CTC TTC TAC ACC ATG AAA GCC GCT CTG GGG CTG AAA CCG CCT	1441
	Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro	
	440 445 450	
	AGC GCT GAC GTG TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA	1486
	Ser Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro	
	455 460 465	
50	GTC GAC AAC TTC GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG	1531
	Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln	
	470 475 480	
55	GTC GCC GCG TAC CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA	1576
	Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly	
	485 490 495	
60	TGG GCT GAG TAC ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG CGC	1621
	Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg	
	500 505 510	

5 TAC TCT GTA ATC CAC GGC AAG GAA TAC TTT TCC GAA GGT ACC GCC 1666  
 Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala  
 515 520 525

10 TAC CCA GTT GGT GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC TAC 1711  
 Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr  
 530 535 540

15 ACT ATT GGA GGT GTG ACC CAG GAG GGT GTA TTC AAC GTA CTC TCC 1756  
 Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser  
 545 550 555

20 ACT GAC AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC 1801  
 Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp  
 560 565 570

25 GAG GAC AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA 1846  
 Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg  
 575 580 585

30 AGC ATG GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC 1891  
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr  
 590 595 600

35 CTT ATC GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT 1936  
 Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser  
 605 610 615

40 GAC TTC TCT GAA GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT 1981  
 Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser  
 620 625 630

45 CAC CCG CAG TTC GAA AAA TAATAAGCTT 2009  
 His Pro Gln Phe Glu Lys  
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<210> 18

40 <211> 2005 bases pairs

<212> DNA

<213> fragment of plasmid PBBP29

<220>

45 <221> sig\_peptide

<222> (22)...(84)

<220>

<221> mat\_peptide

50 <222> (85)...(1998)

<223> fusion protein of mutein DigA16, Strep-Tag II, linker peptide Gly(5) and alkaline phosphatase

<220>

5 <221> CDS

<222> (85)...(606)

<223> mutein DigA16

<220>

10 <221> CDS

<222> (607)...(636)

<223> Strep-Tag II affinity tag

<220>

15 <221> CDS

<222> (637)...(651)

<223> linker peptide Gly-Gly-Gly-Gly-Gly

<220>

20 <221> CDS

<222> (652)...(1998)

<223> alkaline phosphatase without signalling sequence and N-terminal Arg

<400> 18

25

TCTAGATAAC GAGGGCAAAA A ATG AAA AAG ACA GCT ATC GCG ATT 45  
Met Lys Lys Thr Ala Ile Ala Ile  
-21 -20 -15

30

GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GAC GTG 90  
Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val  
-10 -5 -1 1

35

TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC 135  
Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe  
5 10 15

40

GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG GTC GCC GCG TAC 180  
Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr  
20 25 30

CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC 225  
Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr  
35 40 45

45



	TAC	ACT	CAC	TAT	GCG	CTG	AAT	AAA	AAA	ACC	GGC	AAA	CCG	GAC	TAC	945
	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	Thr	Gly	Lys	Pro	Asp	Tyr	
			275					280					285			
5	GTC	ACC	GAC	TCG	GCT	GCA	TCA	GCA	ACC	GCC	TGG	TCA	ACC	GGT	GTC	990
	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	Trp	Ser	Thr	Gly	Val	
			290					295					300			
10	AAA	ACC	TAT	AAC	GGC	GCG	CTG	GGC	GTC	GAT	ATT	CAC	GAA	AAA	GAT	1035
	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	His	Glu	Lys	Asp	
			305					310					315			
15	CAC	CCA	ACG	ATT	CTG	GAA	ATG	GCA	AAA	GCC	GCA	GGT	CTG	GCG	ACC	1080
	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	Lys	Ala	Ala	Gly	Leu	Ala	Thr	
			320					325					330			
20	GGT	AAC	GTT	TCT	ACC	GCA	GAG	TTG	CAG	GAT	GCC	ACG	CCC	GCT	GCG	1125
	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	Thr	Pro	Ala	Ala	
			335					340					345			
25	CTG	GTG	GCA	CAT	GTG	ACC	TCG	CGC	AAA	TGC	TAC	GGT	CCG	AGC	GCG	1170
	Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	Pro	Ser	Ala	
			350					355					360			
30	ACC	AGT	GAA	AAA	TGT	CCG	GGT	AAC	GCT	CTG	GAA	AAA	GGC	GGA	AAA	1215
	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	Gly	Lys	
			365					370					375			
35	GGA	TCG	ATT	ACC	GAA	CAG	CTG	CTT	AAC	GCT	CGT	GCC	GAC	GTT	ACG	1260
	Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	Thr	
			380					385					390			
40	CTT	GGC	GGC	GGC	GCA	AAA	ACC	TTT	GCT	GAA	ACG	GCA	ACC	GCT	GGT	1305
	Leu	Gly	Gly	Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	
			395					400					405			
45	GAA	TGG	CAG	GGA	AAA	ACG	CTG	CGT	GAA	CAG	GCA	CAG	GCG	CGT	GGT	1350
	Glu	Trp	Gln	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	
			410					415					420			
50	TAT	CAG	TTG	GTG	AGC	GAT	GCT	GCC	TCA	CTG	AAT	TCG	GTG	ACG	GAA	1395
	Tyr	Gln	Leu	Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	
			425					430					435			
55	GCG	AAT	CAG	CAA	AAA	CCC	CTG	CTT	GGC	CTG	TTT	GCT	GAC	GGC	AAT	1440
	Ala	Asn	Gln	Gln	Lys	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	
			440					445					450			
60	ATG	CCA	GTG	CGC	TGG	CTA	GGA	CCG	AAA	GCA	ACG	TAC	CAT	GGC	AAT	1485
	Met	Pro	Val	Arg	Trp	Leu	Gly	Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	
			455					460					465			
65	ATC	GAT	AAG	CCC	GCA	GTC	ACC	TGT	ACG	CCA	AAT	CCG	CAA	CGT	AAT	1530
	Ile	Asp	Lys	Pro	Ala	Val	Thr	Cys	Thr	Pro	Asn	Pro	Gln	Arg	Asn	
			470					475					480			
70	GAC	AGT	GTA	CCA	ACC	CTG	GCG	CAG	ATG	ACC	GAC	AAA	GCC	ATT	GAA	1575
	Asp	Ser	Val	Pro	Thr	Leu	Ala	Gln	Met	Thr	Asp	Lys	Ala	Ile	Glu	
			485					490					495			



[illegible]